

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Needleman, Philip
Glenn, Kevin
- (ii) TITLE OF INVENTION: An Immunological Process and Constructs
for Increasing the HDL Cholesterol Concentration by DNA
Vaccination
- (iii) NUMBER OF SEQUENCES: 52
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Welsh & Katz, Ltd.
 - (B) STREET: 120 South Riverside Plaza, 22nd Floor
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gamson Ph.D., Edward P.
 - (B) REGISTRATION NUMBER: 29,381
 - (C) REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (312)655-1500
 - (B) TELEFAX: (312)655-1501

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (viii) POSITION IN GENOME:
 - (C) UNITS: bp
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Drayna, Dennis
Jarnagin, Alisha Stephens
McLean, John
Henzel, William
Kohr, William
Fielding, Christopher
Lawn, Richard

0034367 09199
256760 2924600

(B) TITLE: Cloning and sequencing of human cholesteryl
ester transfer protein cDNA
(C) JOURNAL: Nature
(D) VOLUME: 327
(F) PAGES: 632-634
(G) DATE: June 18-1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA GCCTGCCCTC	60
CTGGTGTGA ACCACGAGAC TGCCAAGGTC ATCCAGACCG CCTTCCAGCG AGCCAGCTAC	120
CCAGATATCA CGGGCGAGAA GGCCATGATG CTCCTTGGCC AAGTCAAGTA TGGGTTGCAC	180
AACATCCAGA TCAGCCACTT GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG	240
TCCATTGATG TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC	300
TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT CGACTCTGCC	360
ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG GTAGAGTGCG GACCGATGCC	420
EETGACTGET ACCTGTCTTT CCATAAGCTG CTCCTGCATC TCCAAGGGGA GCGAGAGCCT	480
GGGTGGATCA AGCAGCTGTT CACAAATTTC ATCTCCTTCA CCCTGAAGCT GGTCTGAAG	540
GGACAGATCT GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA	600
AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT GACAGGTGAT	660
CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG GTCATTTTCAT CTACAAGAAT	720
GTCTCAGAGG ACCTCCCCCT CCCCACCTTC TCGCCACAC TGCTGGGGGA CTCCCGCATG	780
CTGTACTTCT GGTTCTCTGA GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT	840
GGCCGCCTCA TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC	900
TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTGCGCG GCTTCCCCAG CCAGGCCCAA	960
GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC AAAACAAGGG AGTCGTGGTC	1020
AATTCTTCAG TGATGGTGAA ATTCTCTTT CCACGCCAG ACCAGCAACA TTCTGTAGCT	1080
TACACATTTG AAGAGGATAT CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC	1140
TTCTTAAGCC TCTTGATTT CCAGATTACA CCAAAGACTG TTTCCAACCT GACTGAGAGC	1200
AGCTCCGAGT CCATCCAGAG CTTCTGCAG TCAATGATCA CCGCTGTGGG CATCCCTGAG	1260
GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA ACAGCAAAGG CGTGAGCCTC	1320
TTTGACATCA TCAACCCTGA GATTATCACT CGAGATGGCT TCCTGTGCT GCAGATGGAC	1380
TTTGGCTTCC CTGAGCACCT GCTGGTGGAT TTCCTCCAGA GCTTGAGCTA G	1431

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

08031367 091997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln
 1 5 10 15
 Val Ala Val His
 20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
 1 5 10 15
 Ala Tyr Arg Phe
 20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp
 1 5 10 15
 Phe Leu Gln Ser Leu Ser)
 20

is part of seq. 50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu
 1 5 10 15
 Leu Asp Phe Gln
 20

08934367 091997 26150 2946680

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln
1 5 10 15
Leu Phe Thr Asn
 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu Gly Arg Val Lys Tyr
1 5 10 15
Gly Leu His Asn
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
1 5 10 15
Val Thr Val His
 20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Tyr Thr Phe
20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Phe Leu Gln Ser Leu Ser
20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Asp Phe Gln
20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

GTCGCCGTGA CGTTCGCTT CCCCCGCCCA GATGGCCGAG AAGCTGTGGC CTACAGGTTT 60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCTGCTGC AGATGGACTT CGGTTTTCCT AAGCACCTGC TGGTGGATT CTGCAGAGC 60
CTGAGC 65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCACCGTCC AGGCCTCCTA CTCCCAGAAA AAGCTCTTCC TACACCTCTT GGATTTCAG 60

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCTCCTGC ACCTCCAGGG GGAGCGCGAG CCGGGGTGGC TCAAGCAGCT CTTACAAAC 60

20040327 104997 29242680

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
 - (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACGTCAGCG GCGAGAGGGC CGTGATGCTC CTCGGCCGGG TCAAGTACGG GCTGCACAAC 60

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
 - (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGAAATCT TCCAAGAGGT TGTCGGCGGC TTCCCCAGCC AGGCCCAAGT CACCGTCCAC 60
TGC 63

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
 - (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGATGGTGA AATTCCTCTT TCCACGCCCA GACCAGCAAC ATTCTGTAGC TTACACATT 60

08034367 091997
250160 290100

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(viii) POSITION IN GENOME:
(C) UNITS: bp

CTGCTGCTGC AGATGGACTT TGGCTTCCCT GAGCACCTGC TGGTGGATT T CCTCCAGAGC 60
TTGAGC 66

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: ~~nucleic acid~~
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(viii) POSITION IN GENOME:
(C) UNITS: bp

ACTACCGTCC AGGCCTCCTA TTCTAAGAAA AAGCTCTTCT TAAGCCTCTT GGATTTCCAG 60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(viii) POSITION IN GENOME:
(C) UNITS: bp

CTGCTCCTGC ATCTCCAAGG GGAGCGAGAG CCTGGGTGGA TCAAGCAGCT GTTCACAAAT 60

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATATCACGG GCGAGAAGGC CATGATGCTC CTTGGCCAAG TCAAGTATGG GTTGACAAAC 60

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Nagashima, M.
McLean, J. W.
Lawn, R. M.
- (B) TITLE: Cloning and mRNA tissue distribution of
rabbit cholesteryl ester transfer protein
- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (F) PAGES: 1643-1649
- (G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Cys	Pro	Lys	Gly	Ala	Ser	Tyr	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile	1	5	10	15
Thr	Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val	20	25	30	
Gln	Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg	35	40	45	
Ala	Val	Met	Leu	Leu	Gly	Arg	Val	Lys	Tyr	Gly	Leu	His	Asn	Leu	Gln	50	55	60	
Ile	Ser	His	Leu	Ser	Ile	Ala	Ser	Ser	Gln	Val	Glu	Leu	Val	Asp	Ala	65	70	75	
Lys	Thr	Ile	Asp	Val	Ala	Ile	Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly	85	90	95	
Thr	Leu	Asn	Tyr	Ser	Tyr	Thr	Ser	Ala	Trp	Gly	Leu	Gly	Ile	Asn	Gln	100	105	110	
Ser	Val	Asp	Phe	Glu	Ile	Asp	Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	115	120	125	

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Glu Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
 130 135 140
 Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu
 145 150 155 160
 Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu
 165 170 175
 Lys Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser
 180 185 190
 Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser
 195 200 205
 Asp Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile
 210 215 220
 Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys
 225 230 235 240
 Asn Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu
 245 250 255
 Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn
 260 265 270
 Ser Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu
 275 280 285
 Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr
 290 295 300
 Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln
 305 310 315 320
 Ala Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln
 325 330 335
 Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
 340 345 350
 Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp
 355 360 365
 Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu
 370 375 380
 His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser
 385 390 395 400
 Ser Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser
 405 410 415
 Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser
 420 425 430
 Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val
 435 440 445
 Ala Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile
 450 455 460
 Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met
 465 470 475 480
 Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu
 485 490 495
 Ser

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Nagashima, Mariko
McLean, John W.
Lawn, Richard M.
- (B) TITLE: Cloning and mRNA tissue distribution of
rabbit cholesteryl ester transfer protein
- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (F) PAGES: 1643-1649
- (G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCTGTCCCA AAGGCGCCTC CTACGAGGCT GGCATCGTGT GTCGCATCAC CAAGCCCCGCC	60
CTCTTGGTGT TGAACCAAGA GACGGCCAAG GTGGTCCAGA CGGCCTTCCA GCGCGCCGGC	120
TATCCGGACG TCAGCGGCGA GAGGGCCGTG ATGCTCCTCG GCCGGGTCAA GTACGGGCTG	180
CACAACCTCC AGATCAGCCA CCTGTCCATC GCCAGCAGCC AGGTGGAGCT GGTGGACGCC	240
AAGACCATCG ACGTCGCCAT CCAGAACGTG TCCGTGGTCT TCAAGGGGAC CCTGAACTAC	300
AGCTACACGA GTGCCTGGGG GTTGGGCATC AATCAGTCTG TCGACTTCGA GATCGACTCT	360
GCCATTGACC TCCAGATCAA CACAGAGCTG ACCTGCGACG CTGGCAGTGT GCGCACCAAT	420
GCCCCGACT GCTACCTGGC TTTCCATAAA CTGCTCCTGC ACCTCCAGGG GGAGCGCGAG	480
CCGGGGTGGC TCAAGCAGCT CTTCAAAAC TTCATCTCCT TCACCCTGAA GCTGATTCTG	540
AAGCGACAGG TCTGCAATGA GATCAACACC ATCTCCAACA TCATGGCTGA CTTTGTCCAG	600
ACGAGGGCCG CCAGCATCCT CTCAGATGGA GACATCGGGG TGGACATTTC CGTGACGGGG	660
GCCCCTGTCA TCACAGCCAC CTACCTGGAG TCCCATCACA AGGGTCACTT CACGCACAAG	720
AACGTCTCCG AGGCCTTCCC CCTCCGCGCC TTCCCGCCCG GTCTTCTGGG GGACTCCCGC	780
ATGCTCTACT TCTGGTTCTC CGATCAAGTG CTCAACTCCC TGGCCAGGGC CGCCTTCCAG	840
GAGGGCCGTC TCGTGCTCAG CCTGACAGGG GATGAGTTCA AGAAAGTGCT GGAGACCCAG	900
GGTTTCGACA CCAACCAGGA AATCTTCCAG GAGCTTTCCA GAGGCCTTCC CACCGGCCAG	960
GCCCAGGTAG CCGTCCACTG CCTTAAGGTG CCCAAGATCT CCTGCCAGAA CCGGGGTGTC	1020
GTGGTGTTCTT CTTCCGTGCG CGTGACGTTT CGCTTCCCCC GCCCAGATGG CCGAGAAGCT	1080
GTGGCCTACA GGTTTGAGGA GGATATCATC ACCACCGTCC AGGCCTCCTA CTCCCAGAAA	1140
AAGCTCTTCC TACACCTCTT GGATTTCCAG TCGTGCCGG CCAGCGGAAG GGCAGGCAGC	1200

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- 09-07-06 08:43:03

- 09-07-2008 16:43:03

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- [illegible]

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Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
165 170 175

Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn
180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr
210 215 220

Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn
225 230 235 240

Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly
245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser
260 265 270

Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met
275 280 285

Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn
290 295 300

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
305 310 315 320

Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys
325 330 335

Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg
340 345 350

Pro Asp Gln Gln His Ser Val Ala Tyr Tyr Phe Glu Glu Asp Ile Val
355 360 365

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu
370 375 380

Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser
385 390 395 400

Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu
420 425 430

Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile
435 440 445

Ile Thr Arg Asp Gly Phe Leu Leu Gln Met Asp Phe Gly Phe Pro
450 455 460

Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
465 470 475

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

266760" 2944580

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Swenson, T. L.
et al.,
(C) JOURNAL: J. Biol. Chem.
(D) VOLUME: 264
(F) PAGES: 14318-14326
(G) DATE: 1989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His
1 5 10 15

Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Pape, Michael E.
Rehberg, Edward F.
Marotti, Keith R.
Melchior, George W.
(B) TITLE: Molecular Cloning, Sequence, and Expression
of Cynomolgus Monkey Cholesteryl Ester Transfer
Protein
(C) JOURNAL: Arteriosclerosis and Thrombosis
(D) VOLUME: 11
(E) ISSUE: 6
(F) PAGES: 1759-1771
(G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly Asn Val His
1 5 10 15

Ala Cys Ser Lys Gly Thr Ser His Lys Ala Gly Ile Val Cys Arg Ile
20 25 30

Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Ile
35 40 45

Gln Ser Ala Phe Gln Arg Ala Asn Tyr Pro Asn Ile Thr Gly Glu Lys
50 55 60

Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln
65 70 75 80

Ile Ser His Leu Ser Ile Ala Ser Ser Arg Val Glu Leu Val Glu Ala
85 90 95

Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly
100 105 110

Thr Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Gly Leu Gly Ile Asp Gln
115 120 125

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Ser Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr
130 135 140

Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
145 150 155 160

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu
165 170 175

Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu
180 185 190

Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Ile Ile Ser
195 200 205

Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser
210 215 220

Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Ile Ile
225 230 235 240

Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly Tyr Phe Ile Tyr Lys
245 250 255

Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Ala Leu Leu
260 265 270

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Gln Val Phe His
275 280 285

Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Thr Leu Ser Leu
290 295 300

Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr
305 310 315 320

Asn Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala
325 330 335

Gln Val Thr Val His Cys Leu Lys Met Pro Arg Ile Ser Cys Gln Asn
340 345 350

Lys Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
355 360 365

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile
370 375 380

Met Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser
385 390 395 400

Leu Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu
405 410 415

Ser Ser Ser Glu Ser Val Gln Ser Phe Leu Gln Ser Met Ile Thr Thr
420 425 430

Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Ala Val Phe Thr Ala
435 440 445

Leu Met Asn Ser Lys Gly Leu Ser Leu Phe Asp Ile Ile Asn Pro Glu
450 455 460

Ile Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe
465 470 475 480

Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
485 490

20250403 094367

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Pape, Michael E.
Rehberg, Edward F.
Marotti, Keith R.
Melchior, George W.
- (B) TITLE: Molecular Cloning, Sequence, and Expression
of Cynomolgus Monkey Cholesteryl Ester Transfer
Protein
- (C) JOURNAL: Arteriosclerosis and Thrombosis
- (D) VOLUME: 11
- (E) ISSUE: 6
- (F) PAGES: 1759-1771
- (G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGGCTG CCACCGTCCT GACCCTGGCC CTGCTGGGCA ATGTCCACGC CTGCTCCAAA	60
GGTACCTCAC ACAAGGCAGG CATTGTGTGC CGCATCACCA AGCCTGCCCT CCTGGTGTTC	120
AACCAACAGA CTGCCAAGGT GATCCAGTCT GCCTTCCAGC GAGCCAACTA CCCAAATATC	180
ACAGGCGAGA AGGCCATGAT GCTCCTTGGC CAAGTCAAGT ATGGGTTGCA CAACATCCAA	240
ATCAGCCACT TGTCCATCGC CAGCAGCCGG GTGGAGCTGG TGAAGCCAA GTCCATTGAT	300
GTCTCCATTC AGAACGTGTC TGTGGTCTTC AAGGGGACCC TGAAGTATGG CTACACCACT	360
GCCTGGGGGC TGGGCATTGA TCAGTCCGTT GACTTCGAGA TCGACTCTGC CATTGACCTC	420
CAGATCAACA CACAACTGAC CTGTGACTCT GGTAGAGTGA GGACTGATGC CCCTGACTGC	480
TACCTGTCTT TCCATAAGCT GCTCCTGCAT CTCCAAGGGG AGCGAGAGCC CGGGTGGATC	540
AAGCAGCTGT TCACAAACTT CATCTCCTTC ACCCTGAAGC TGGTCTGAA GGGACAGATC	600
TGCAAAGAGA TCAACATCAT CTCCAACATC ATGGCCGATT TTGTCCAGAC AAGGGCTGCC	660
AGTATCCTTT CAGATGGAGA CATCGGGGTG GACATTTCCC TGACAGGTGA TCCCATCATT	720
ACAGCCTCCT ACCTGGAGTC CCATCACAAG GGTTATTTC TCTATAAGAA TGTCTCGGAG	780
GACCTCCCAC TCCCCACCTT CTCGCCCGCA CTGCTGGGGG ACTCCCGCAT GCTGTACTTC	840
TGGTTCTCCG AGCAAGTCTT CCACTCCCTG GCCAAGGTAG CTTTCCAAGA TGCCCGCCTC	900
ACGCTCAGCC TGATGGGAGA CGAGTTCAAG GCAGTGCTGG AGACCTGGGG CTTCAACACC	960
AACCAAGAAA TCTTCCAGGA GGTTGTCGGC GGCTTCCCA GCCAGGCCA AGTCACCGTC	1020
CACTGCCTCA AGATGCCCAG GATCTCCTGC CAAAACAAGG GAGTCGTGGT CAATTCCTTCG	1080
GTGATGGTGA AATTCCTCTT TCCACGCCA GACCAGCAAC ACTCTGTAGC TTACACATTT	1140
GAAGAGGATA TCATGACCAC CGTCCAGGCC TCCTATTCTA AGAAAAAGCT CTTCTTAAGC	1200
CTCTTGATT TCCAGATTAC ACCAAAGACT GTTTCCAAC TGAAGTGGAG CAGCTCCGAG	1260

08934367 091997

TCCGTCAG GCTTCCTGCA GTCAATGATC ACCACTGTGG GCATCCCTGA GGTCATGTCT 1320
 CGGCTTGAGG CAGTGTTTAC AGCCCTCATG AACAGCAAAG GCCTGAGCCT CTTGACATC 1380
 ATCAATCCTG AGATTATCAC TCGAGATGGC TTCCTGCTGC TGCAGATGGA CTTTGGCTTC 1440
 CCTGAGCACC TGCTGGTGA TTTCTCCAG AGCTTGAGCT AGAAGTCTCC AAGGACGTCA 1500
 GGATGGGG 1508

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
 1 5 10 15
 Val Thr Val His
 20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val
 1 5 10 15
 Ala Tyr Thr Phe
 20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp
 1 5 10 15

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(2) INFORMATION FOR SEQ ID NO:35:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu
1 5 10 15
Leu Asp Phe Gln
20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln
1 5 10 15
Leu Phe Thr Asn
20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asn Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr
1 5 10 15
Gly Leu His Asn
20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50           55           60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65           70           75           80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
          85           90           95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
          100          105          110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
          115          120          125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
          130          135          140
Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
          145          150          155          160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
          165          170          175
Gln Ser Arg Glu Ser Gln Cys
          180
  
```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

ATGGACATCG ACCCTTATAA AGAATTTGGA GCTACTGTGG AGTTACTCTC GTTTTTGCCT      60
TCTGACTTCT TTCCTTCAGT ACGAGATCTT CTAGATACCG CCTCAGCTCT GTATCGGGAA      120
  
```

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(2) INFORMATION FOR SEQ ID NO:40:

- (ii) MOLECULE TYPE: peptide

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
1 5 10 15
Val Ser Tyr Val Asn Thr Asn Met Gly
20 25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
1 5 10 15
Ile Glu Tyr Leu Val
20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro
1 5 10 15

Asn Ala Pro Ile Leu
20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCCATGG ACATCGACCC TTATAAAGAA TTTGG

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT TTAACATTGA GATTCCCGAG ATTGAGATCT TCTG

44

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

00934367 1091997 255150 2924580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCGAATTC ACTAGTTGGA AGATCCAGCG TCTAGAGACC TAG

43

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATCGAATTC CTCGAGCTAG AGTCATTAGT TCCCCCAGC A

41

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATTATCACT CGAGATGGCT TCCTGCTGCT GCAG

34

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATCGAATTC AGCGCTCAAG CTCTGGAGGA AATCCACCAG

40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

260760-2944600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His
1 5 10 15
Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
20 25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGCCGCAACG TTTTACTAGC TCAGGCTCTG CAGGAAATCC ACCAGCAGGT G 51

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCCGCCCAT GGCCTGTCCC AAAGGCGCCT CCTACGAGGC T 41

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